AMENDMENTS TO THE CLAIMS

1. (currently amended) A method for assaying homocysteine (Hcy), S-adenosylhomocysteine (SAH) or adenosine in a sample, which method comprises:

a) contacting a sample containing or suspected of containing Hcy, SAH or adenosine with a mutant SAH hydrolase derived from a SAH hydrolase, wherein said SAH hydrolase is encoded by a nucleic acid comprising the nucleotide sequences selected from the group consisting of SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, and SEQ ID NO:188 ~~with the GenBank accession numbers selected from the group consisting of AF129871; AQ003753; AF105295; AA955402; AA900229; AA874914; AA695679; AA803942; AI187655; U40872; AJ007835; AF080546; AI069796; Z97059; AF059581; U82761; AA754430; D49804; D45204; X95636; T18277; R75259; Z26881; X12523; X64391; W21772; AH003443; U14963; U14962; U14961; U14960; U14959; U14937; U14988; U14987; U14986; U14985; U14984; U14983; U14982; U14981; U14980; U14979; U14978; U14977; U14976; U14975; L32836; L35559; Z19779; L23836; M15185; L11872; M19937; M80630; M61831; and M61832~~;

wherein said mutant SAH hydrolase has binding affinity for Hcy, SAH or adenosine but has attenuated catalytic activity, and wherein said binding affinity and/or said attenuated catalytic activity of said mutant SAH hydrolase is caused by a mutation in said mutant SAH hydrolase's catalytic site, its binding site for NAD^+, NADH, Hcy, SAH, adenosine, or a combination thereof; and wherein the mutant SAH hydrolase: i) has a mutation in an amino acid residue that participates in catalysis or that is directly interacting with NAD^+, NADH, Hcy, SAH or adenosine; or ii) has a mutation in an amino acid residue that is adjacent to an amino acid residue that participates in catalysis or that is directly interacting with NAD^+, NADH, Hcy, SAH or adenosine; and

b) detecting binding between Hcy, SAH or adenosine with said mutant SAH hydrolase, whereby the presence or amount of Hcy, SAH or adenosine in said sample is assessed.

2-3. (canceled)

4. (previously presented) The method of claim 1, wherein the mutant SAH hydrolase has at least 50 fold higher binding affinity for Hcy, SAH or adenosine than a wild type SAH hydrolase from which said mutant SAH hydrolase is derived.

5. (canceled)

6. (currently amended) A method for assaying homocysteine (Hcy), S-adenosylhomocysteine (SAH) or adenosine in a sample, which method comprises:

a) contacting a sample containing or suspected of containing Hcy, SAH or adenosine with a mutant SAH hydrolase, wherein the mutant SAH hydrolase is derived from a human SAH hydrolase comprising the amino acid sequence set forth in SEQ ID NO:1, wherein said mutant SAH hydrolase has binding affinity for Hcy, SAH or adenosine but has attenuated catalytic activity, and wherein said binding affinity and/or said attenuated catalytic activity of said mutant SAH hydrolase is caused by a mutation in said mutant SAH hydrolase's catalytic site, its binding site for NAD^+, NADH, Hcy, SAH, adenosine, or a combination thereof; and wherein the mutant SAH hydrolase: i) has a mutation in an amino acid residue that participates in catalysis or that is directly interacting with NAD^+, NADH, Hcy, SAH or adenosine; or ii) has a mutation in an amino acid residue that is adjacent to an amino acid residue that participates in catalysis or that is directly interacting with NAD^+, NADH, Hcy, SAH or adenosine; and

b) detecting binding between Hcy, SAH or adenosine with said mutant SAH hydrolase, whereby the presence or amount of Hcy, SAH or adenosine in said sample is assessed.

7. (previously presented) The method of claim 6, wherein the mutant SAH hydrolase comprises the amino acid sequence set forth in SEQ ID NO:1 and comprises a mutation selected from the group consisting of R38E, C53S, L54G, T57G, T57S, E59D, N80G, S83G, Y100T, K121A, D131E, D134E, E155G, T157G, T158Y, T159Y, N181A, N191A, L214A, Y221S, K226A, F235S, I240L, N248A, D263G, G269D, R285D, D292G, H301T, K309R, K322G, R329A, L347F, L347Y, L347I, M351A, H353R, S361G, F362S, Y379S, L386A, K388G, H398A, K401R, K401D,

T407S, L409G, S420T, P424A, F425S, P427A, D428G, H429A, Y430T, R431K, R431G, Y432S, Y432A, Y432F, and a combination thereof.

8. (previously presented) The method of claim 1, wherein prior to the contact between the sample and the mutant SAH hydrolase, oxidized or conjugated Hcy in the sample is converted into reduced Hcy by a reducing agent.

9. (original) The method of claim 1, wherein prior to the contact between the sample and the mutant SAH hydrolase, the Hcy in the sample is converted into SAH.

10-12. (canceled)

13. (previously presented) The method of claim 8, further comprising a step of removing the reducing agent used to convert oxidized or conjugated Hcy into reduced Hcy prior to or concurrently with contacting the sample with the mutant SAH hydrolase, wherein the reducing agent is removed by chromatography.

14-17. (canceled)

18. (previously presented) The method of claim 1, wherein the sample is contacted with the mutant SAH hydrolase in the presence of a labeled SAH, a labeled SAH derivative, or a labeled SAH analogue, thereby the amount of the labeled SAH, SAH derivative, or SAH analogue bound to the mutant SAH hydrolase inversely relates to the amount of SAH in the sample.

19. (previously presented) The method of claim 18, wherein the labeled SAH, SAH derivative, or SAH analogue is labeled with a fluorophore, an enzyme, or a protein.

20-22. (canceled)

23. (original) The method of claim 1, wherein the mutant SAH hydrolase is a labeled mutant SAH hydrolase.

24. (original) The method of claim 23, wherein the labeled mutant SAH is a fluorescently, enzymatically, biotin or streptavidin labeled mutant SAH hydrolase.

25-27. (canceled)

28. (previously presented) The method of claim 19, wherein the fluorophore labeled SAH, SAH derivative, or SAH analogue is directly contacted by the mutant SAH hydrolase, and the resulting change of fluorescent polarization is measured for assessing the presence or amount of Hcy, SAH or adenosine in the sample.

29. (previously presented) The method of claim 19, wherein the enzyme labeled SAH, SAH derivative, or SAH analogue is directly contacted by the mutant SAH hydrolase, and the resulting change of enzyme activity is measured for assessing the presence or amount of Hcy, SAH or adenosine in the sample.

30. (original) The method of claim 1, wherein the mutant SAH hydrolase is immobilized.

31. (original) The method of claim 1, wherein the sample is a body fluid or a biological tissue.

32-35. (canceled)

36. (withdrawn) A combination, which combination comprises:

a) a mutant SAH hydrolase that has binding affinity for Hcy, SAH or adenosine but has attenuated catalytic activity, wherein said binding affinity and/or said attenuated catalytic activity of

said SAH hydrolase is caused by a mutation in said mutant SAH hydrolase's catalytic site, its binding site for NAD^+, NADH, Hcy, SAH or adenosine, or a combination thereof; and

b) reagents for detecting binding between Hcy, SAH or adenosine and said SAH hydrolase.

37. (withdrawn) The combination of claim 36, further comprising a reagent for detecting cholesterol and/or folic acid.

38. (withdrawn) A kit, which kit comprises the combination of claim 36.

39. (withdrawn) The kit of claim 38, further comprising instructions for assaying Hcy, SAH or adenosine in a sample.

40. (withdrawn) An article of manufacture, which article of manufacture comprises:

a) packaging material;

b) a mutant SAH hydrolase that has binding affinity for Hcy, SAH or adenosine but has attenuated catalytic activity, wherein said binding affinity and/or said attenuated catalytic activity of said SAH hydrolase is caused by a mutation in said mutant SAH hydrolase's catalytic site, its binding site for NAD^+, NADH, Hcy, SAH or adenosine, or a combination thereof; and

c) a label indicating that the mutant SAH hydrolase and the means for use in assaying Hcy in a sample.

41. (withdrawn) An isolated nucleic acid fragment, which isolated nucleic acid fragment comprises a sequence of nucleotides encoding a mutant SAH hydrolase, wherein said mutant SAH hydrolase comprises the amino acid sequence set forth in SEQ ID NO:1 and comprises a mutation selected from the group consisting of R38E, C53S, L54G, T57G, T57S, E59D, N80G, S83G, Y100T, K121A, D131E, D134E, E155G, T157G, T158Y, T159Y, N181D, N181A, D190A, N191A, L214A, Y221S, K226A, F235S, I240L, N248A, D263G, G269D, R285D, D292G, H301T, K309R, K322G, R329A, L347F, L347Y, L347I, M351A, H353R, S361G, F362S, Y379S, L386A,

K388G, H398A, K401R, K401D, T407S, L409G, S420T, P424A, F425S, P427A, D428G, H429A, Y430T, R431K, R431G, Y432S, Y432A, Y432F, and a combination thereof.

42. (withdrawn) The isolated nucleic acid fragment of claim 41, wherein the nucleic acid is DNA.

43. (withdrawn) The isolated nucleic acid fragment of claim 41, wherein the nucleic acid is RNA.

44. (withdrawn) A plasmid, which plasmid comprises the nucleic acid fragment of claim 41.

45. (withdrawn) A cell, which cell comprises the plasmid of claim 44.

46. (withdrawn) The cell of claim 45 selected from the group consisting of a bacterial cell, a yeast cell, a fungal cell, a plant cell, an insect cell and an animal cell.

47. (withdrawn) A method for producing a mutant SAH hydrolase, which method comprises growing the cell of claim 45 under conditions whereby the mutant SAH hydrolase is expressed by the cell, and recovering the expressed mutant SAH hydrolase.

48. (withdrawn) A substantially purified mutant SAH hydrolase, wherein said mutant SAH hydrolase comprises the amino acid sequence set forth in SEQ ID NO:1 and comprises a mutation selected from the group consisting of R38E, C53S, L54G, T57G, T57S, E59D, N80G, S83G, Y100T, K121A, D131E, D134E, E155G, T157G, T158Y, T159Y, N181D, N181A, D190A, N191A, L214A, Y221S, K226A, F235S, I240L, N248A, D263G, G269D, R285D, D292G, H301T, K309R, K322G, R329A, L347F, L347Y, L347I, M351A, H353R, S361G, F362S, Y379S, L386A, K388G, H398A, K401R, K401D, T407S, L409G, S420T, P424A, F425S, P427A, D428G, H429A, Y430T, R431K, R431G, Y432S, Y432A, Y432F, and a combination thereof.

49. (withdrawn) A conjugate, which conjugate comprises:

a) a mutant SAH hydrolase that has binding affinity for Hcy, SAH or adenosine but has attenuated catalytic activity, wherein said binding affinity and/or said attenuated catalytic activity of said SAH hydrolase is caused by a mutation in said mutant SAH hydrolase's catalytic site, its binding site for NAD^+, NADH, Hcy, SAH or adenosine, or a combination thereof; and

b) a facilitating agent linked to the mutant SAH hydrolase directly or via a linker, wherein the agent facilitates:

i) affinity isolation or purification of a conjugate;

ii) attachment of a conjugate to a surface; or

iii) detection of a conjugate.

50. (withdrawn) The conjugate of claim 49, which is a fusion protein.

51. (cancelled)

52. (previously presented) The method of claim 6, wherein the mutant SAH hydrolase has at least 50 fold higher binding affinity for Hcy, SAH or adenosine than a wild type SAH hydrolase from which said mutant SAH hydrolase is derived.

53. (previously presented) The method of claim 6, wherein the sample is contacted with the mutant SAH hydrolase in the presence of a labeled SAH, a labeled SAH derivative, or a labeled SAH analogue, thereby the amount of the labeled SAH, SAH derivative, or SAH analogue bound to the mutant SAH hydrolase inversely relates to the amount of SAH in the sample.

54. (previously presented) The method of claim 53, wherein the labeled SAH, SAH derivative, or SAH analogue is labeled with a fluorophore, an enzyme, or a protein.

55. (previously presented) The method of claim 6, wherein the mutant SAH hydrolase is a labeled mutant SAH hydrolase.

56. (previously presented) The method of claim 6, wherein the mutant SAH hydrolase is immobilized.